



FIGURE 1A

SEQ ID NO:04	** * * ***** *	MATTSATTAATAA-----ATTAKPRGSSSALCQRVAGGRR-----RSGVVRCDAAAG	** * * * * * * * *
SEQ ID NO:12		MAVSTTFSGAKLEALLLKCSSSSSSPPPSRSS--FTTFPGQNRRTLIQ--RGVIRCDAAQP	
SEQ ID NO:29		MAVSTSPFGAKLEALLLKCGSSNAATATATTTTHLSCFC-KTRKTLVQSQRGPIRCEASS	
		1	60
SEQ ID NO:04	* * * * *	V-EAQQAQAVAKAASVAALAEQFKISA-DRYMKERSTIAVIGLSVHTAPVEMREKLAVAEEL	* * * * *
SEQ ID NO:12		-SDASSVAPNNATALSALEQLKTSAADRYTKERSIIAIGLSVHTAPVEMREKLAIPAE	
SEQ ID NO:29		ASDVVADATKKAASVSALEQLKTSAADRYTKERSVVMVIGLSVHSTPVMREKLAIPAE	
		61	120
SEQ ID NO:04	*****	WPRAIQELTSLNHIIEAAVLSTCNRMEIYVVALSWNRGIREVVDWMSKSGIPASELREH	*****
SEQ ID NO:12		WPRAIAELCSLNHIIEAAVLSTCNRMEIYVVALSQHRGVKEVMEWMSKTSSVPVSELSQH	
SEQ ID NO:29		WPRAIAELCSLNHIIEAAVLSTCNRMEIYVVALSKHRGVKEVTEWMSKTSGIPVADLCQH	
		121	180
SEQ ID NO:04	* * * * *	LFILRSSDATRHLFEVSAGLDSLVLGEGQILAQVKQVVRSGQNSGGLGKNIDRMFKDAIT	* * * * *
SEQ ID NO:12		RFLLYNNDATQHLFEVSAGLDSLVLGEGQILSQVKQVVKVQGQVNGFGRNISGLFKHAIT	
SEQ ID NO:29		QFLLYNKDATQHLFEVSAGLDSLVLGEGQILAQVKQVVKVQGQVNGFGRNISGLFKHAIT	
		181	240
SEQ ID NO:04	*****	AGKRVRETNISSGAVSVSSAAVELALMKLPKSEALSARMLLIGAGKMGKLVIKHLVAKG	*****
SEQ ID NO:12		VGKRVRETNIASGAVSVSSAAVELAYMKLPEASHDNARMLVIGAGKMGKLVIKHLVAKG	
SEQ ID NO:29		VGKRVRETNIAGAVSVSSAAVELALMKLPEASHANARMLVIGAGKMGKLVIKHLVAKG	
		241	300



FIGURE 2A

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*****
SEQ ID NO:26 MAGAAAAAASAAAVASGISARPVAPRPSRARAPRSVVRAAISVEKGEKAYTVEKSEEI *****
SEQ ID NO:30 MAGAAAA-----VASGISIRPVAA-PKISRAPRSRVRAAVSID--EKAYTVQKSEEI *****
1
*****
SEQ ID NO:26 FNAAKELMPGGVNSPVRAFKS VGGQPIVFD SVKGSRMWDVDGNEYIDYVGSWGPAAIIGHA *****
SEQ ID NO:30 FNAAKELMPGGVNSPVRAFKS VGGQPIVFD SVKGSRMWDVDGNEYIDYVGSWGPAAIIGHA *****
61
*****
** *****
SEQ ID NO:26 DDTVNAALIIETLKKGTSFGAPCVLENVLAEMVISAVPSIEMVRFVNSGTEACMGALRLVR *****
SEQ ID NO:30 DDKNVNAALIIETLKKGTSFGAPCALENVLAQMVISAVPSIEMVRFVNSGTEACMGALRLVR *****
121
*****
*****
SEQ ID NO:26 AFTGREKILKFEGCYHGHADSFLVKAGSGVATLGLPDSPGVPKGATSETLTAPYNDVEAV *****
SEQ ID NO:30 AFTGREKILKFEGCYHGHADSFLVKAGSGVATLGLPDSPGVPKGATVGTLTAPYNDADAV *****
181
*****
*****
SEQ ID NO:26 KKLFEENKGQIAAVFLEPVVGNAGFIPQPQGFNLALRDLTKQDGALLVFDEVMTGFRLAY *****
SEQ ID NO:30 KKLFEEDNKGEIAAVFLEPVVGNAGFIPQPQPAFLNALREVTKQDGALLVFDEVMTGFRLAY *****
241
*****
*****
SEQ ID NO:26 GGAQYFGITPDVSTLTKIIGXGLPVGAYGGRKDIMEMVAPAGPMYQAGTILSGNPLAMTA *****
SEQ ID NO:30 GGAQYFGITPDVSTLTKIIGXGLPVGAYGGRKDIMEMVAPAGPMYQAGTILSGNPLAMTA *****
301
*****
```



FIGURE 2B

GIHTLKRLEPGTYDYLDKITGDLVRGVLDAGAKTGHEMCGGHIRGMFGFFFTAGP VHNF
GIHTLKRLEPGTYEYLDKVTGELVRGILDVGAKTGHEMCGGHIRGMFGFFFTAGP VHNF
361 420

GDAKKSDTAKFGRFYRGMLEEGVYLAPSQFEAGFTSLAHTSQDIEKTVEAAAKVLRRI
DDAKKSDTAKFGRFHRGMLEEGVYLAPSQFEAGFTSLAHTTQDIEKTVEAAAEKVLRWI
421 478

SEQ ID NO:26
SEQ ID NO:30

SEQ ID NO:26
SEQ ID NO:30